FROM PHENE TO GENE:
HOW CROP PHYSIOLOGY IS CRUCIAL TO THE DISCOVERY OF RELIABLE GENETIC BASES OF COMPLEX TRAITS

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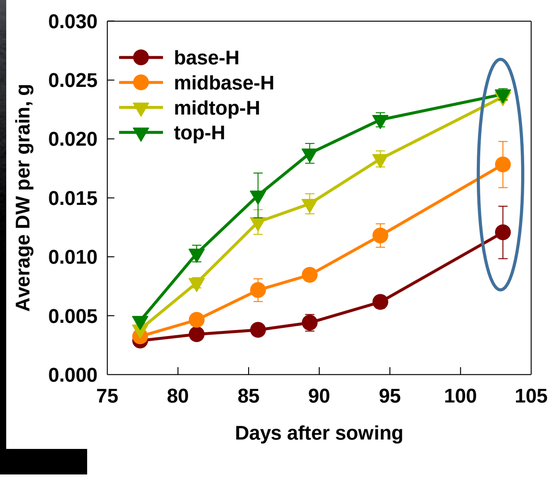
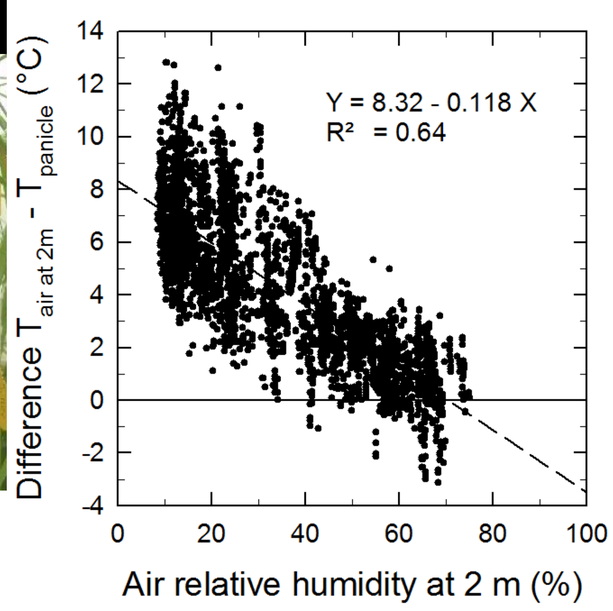
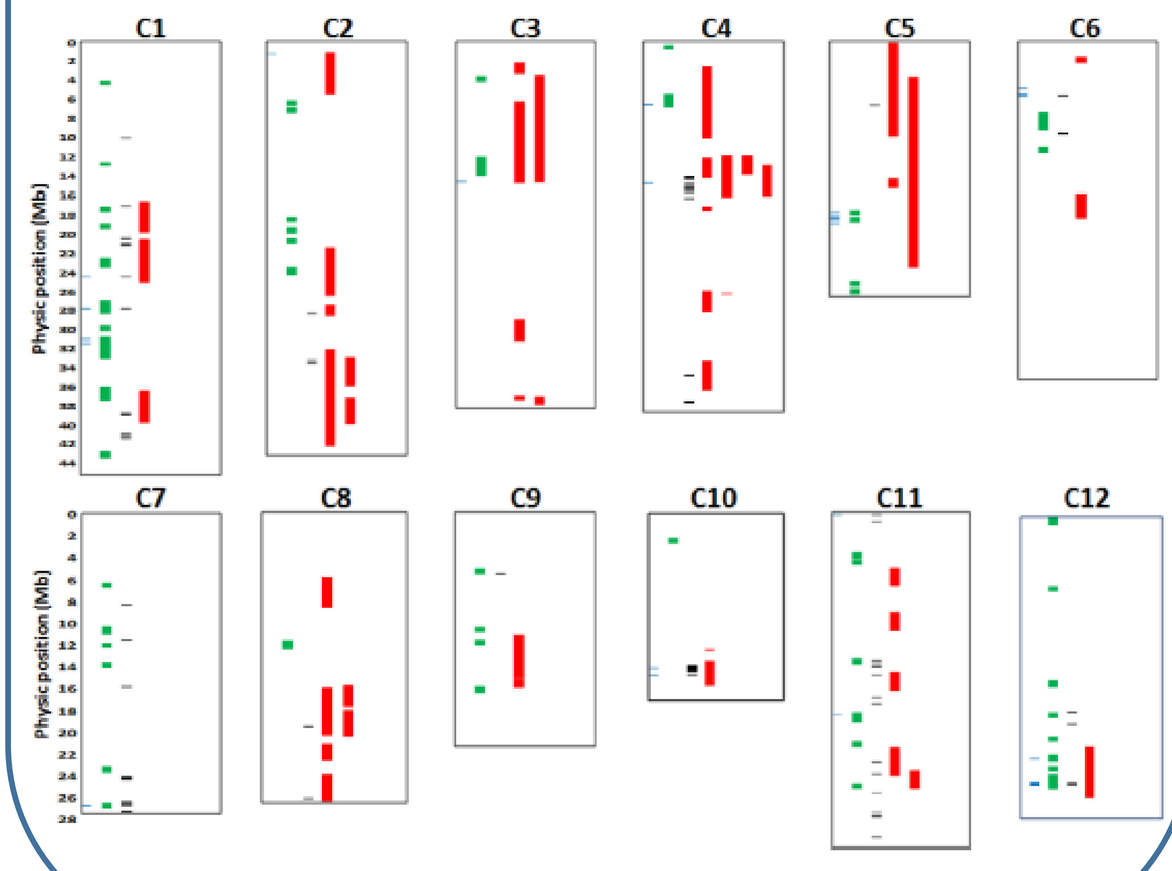
Dissecting the genetic bases of complex traits is one key challenge for improving crop performance and adaptation

High-throughput phenotyping for genome-wide association studies

Quantifying the effect of high temperature on rice spikelet fertility suggests to measure:
- the ratio of filled over unfilled spikelets (**what**)
- only within the top part (**where**) of
- only the panicles that flowers under heat (**where**)
- in response to panicle temperature (**which conditions**)







14 significant independent loci

Julia and Dingkuhn, 2013; Lafarge *et al*, 2017

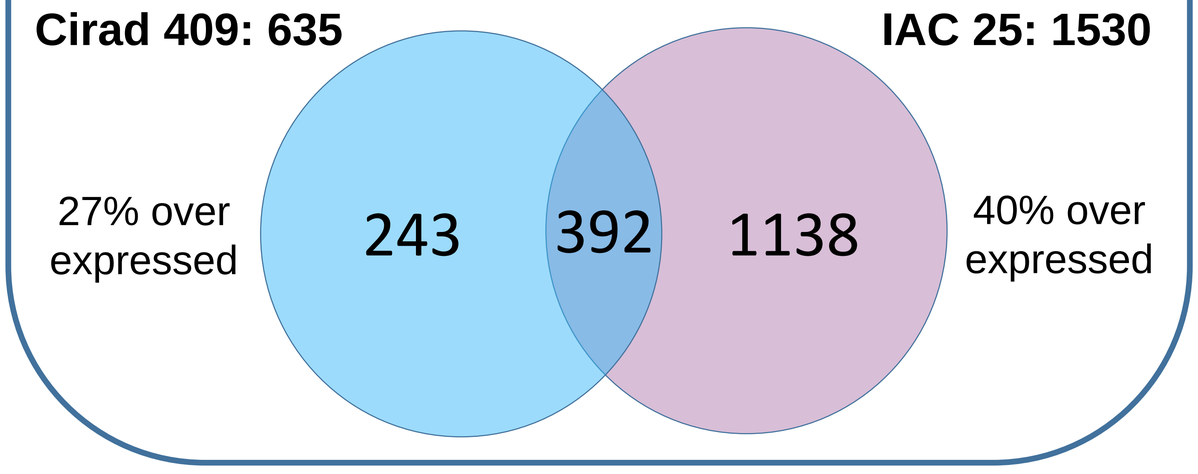
In both cases, gene clustering and ontology allowed to identify associated biological processes consistent with the differential morpho-physiological plant responses

Where crop physiology plays a crucial role:
- which trait(s) (**what**) to measure
- or which organ(s) (**where**) to sample
- at which stage (**when**)
- in **which conditions**

Targeted plant materials sampling of 2 varieties for transcriptomic studies

Quantifying the effect of soil water deficit during the late reproductive phase suggests to measure:
- gene expression of an elongating organ (**what**)
- like internodes (**where**)
- at the same phenological age whatever the genotype (**when**)
- in response to the same available soil water (**which conditions**)

Number of differentially expressed genes in response to water deficit (1%)



In both cases, because of the relevance and rigor of the applied methodology, the major identified genetic bases governing the targeted traits are considered highly reliable